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SEQUENCE LISTING

<110> East Tennessee State University Research Foundation
Lampson, Bert
Vellore, Jashree

<120> RNA-DEPENDENT DNA POLYMERASE FROM GEOBACILLUS STEAROTHERMOPHILUS

<130> 2826067.000002

<140> 10/797,262

<141> 2004-03-10

<160> 12

<170> PatentIn version 3.3

<210> 1

<211> 1263

<212> DNA

<213> Geobacillus stearothermophilus

<220>

<221> CDS

<222> (1)..(1263)

<400> 1

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1 5 10 15	
ctc aaa cgg gtc gaa gcc aac caa gga gca ccg gga atc gac gga gta	96
Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val	
20 25 30	
tca acc gat caa ctc cgt gat tac atc cgc gct cac tgg agc acg atc	144
Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile	
35 40 45	
cgc gcc caa ctc ttg gcg gga acc tac cgg ccg gcg cct gtc cgc agg	192
Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg	
50 55 60	
gtc gga atc ccg aaa ccg ggc ggc ggc aca cgg cag cta ggc att ccc	240
Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro	
65 70 75 80	
acc gtg gtg gac cgg ctg atc caa caa gcc att ctt caa gaa ctc aca	288
Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr	
85 90 95	
ccc att ttc gat cca gac ttc tcc cct tcc agc ttc gga ttc cgt ccg	336
Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro	
100 105 110	
ggc cgt aac gcc cac gat gcc gtg cgg caa gcg caa ggc tac atc cag	384
Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln	
115 120 125	

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gaa ggg tat cgg tac gtg gtc gac atg gac ctg gaa aag ttc ttt gat Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp 130 135 140	432
cgg gtc aac cat gac atc ttg atg agt cgg gtg gcc cga aaa gtc aag Arg Val Asn His Asp Ile Leu Met Ser Arg Val Ala Arg Lys Val Lys 145 150 155 160	480
gat aaa cgc gtg ctg aaa ctg atc cgt gcc tac ctg caa gcc ggc gtt Asp Lys Arg Val Leu Lys Leu Ile Arg Ala Tyr Leu Gln Ala Gly Val 165 170 175	528
atg atc gaa ggg gtg aag gtg cag acg gag gaa ggg acg ccg caa ggc Met Ile Glu Gly Val Lys Val Gln Thr Glu Glu Gly Thr Pro Gln Gly 180 185 190	576
ggc ccc ctc agc ccc ctg ctg gcg aac atc ctt ctc gac gat tta gac Gly Pro Leu Ser Pro Leu Leu Ala Asn Ile Leu Leu Asp Asp Leu Asp 195 200 205	624
aag gaa ttg gag aag cga gga ttg aaa ttc tgc cgt tac gca gat gac Lys Glu Leu Glu Lys Arg Gly Leu Lys Phe Cys Arg Tyr Ala Asp Asp 210 215 220	672
tgc aac atc tat gtg aaa agt ctg cgg gca gga caa cgg gtg aaa caa Cys Asn Ile Tyr Val Lys Ser Leu Arg Ala Gly Gln Arg Val Lys Gln 225 230 235 240	720
agc atc caa cgg ttc ttg gag aaa acg ctc aaa ctc aaa gta aac gag Ser Ile Gln Arg Phe Leu Glu Lys Thr Leu Lys Leu Lys Val Asn Glu 245 250 255	768
gag aaa agt gcg gtg gac cgc ccg tgg aaa cgg gcc ttt ctg ggg ttt Glu Lys Ser Ala Val Asp Arg Pro Trp Lys Arg Ala Phe Leu Gly Phe 260 265 270	816
agc ttc aca ccg gaa cga aaa gcg cga atc cgg ctc gcc cca agg tcg Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala Pro Arg Ser 275 280 285	864
att caa cgt ctg aaa cag cgg att cga cag ctg acc aac cca aac tgg Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn Pro Asn Trp 290 295 300	912
agc ata tcg atg cca gaa cga att cat cgc gtc aat caa tac gtc atg Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln Tyr Val Met 305 310 315 320	960
gga tgg atc ggg tat ttt cgg ctc gtc gaa acc ccg tct gtc ctt cag Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser Val Leu Gln 325 330 335	1008
acc atc gaa gga tgg att cgg agg agg ctt cga ctc tgt caa tgg ctt Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys Gln Trp Leu 340 345 350	1056
caa tgg aaa cgg gtc aga acc aga atc cgt gag tta aga gcg ctg ggg Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg Ala Leu Gly 355	1104

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355	360	365	
ctg aaa gag aca gcg gtg atg gag atc gcc aat acc cga aaa gga gct			1152
Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala			
370	375	380	
tg g cga aca acg aaa acg ccg caa ctc cac cag gcc ctg ggc aaa acc			1200
Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr			
385	390	395	400
tac tgg acc gct caa ggg ctc aag agt ttg acg caa cga tat ttc gaa			1248
Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu			
405	410	415	
ctc cgt caa ggt tga			1263
Leu Arg Gln Gly			
420			

<210> 2
 <211> 420
 <212> PRT
 <213> Geobacillus stearothermophilus

<400> 2

Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu Ile Thr Ala
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Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile Asp Gly Val
 20 25 30

Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp Ser Thr Ile
 35 40 45

Arg Ala Gln Leu Leu Ala Gly Thr Tyr Arg Pro Ala Pro Val Arg Arg
 50 55 60

Val Gly Ile Pro Lys Pro Gly Gly Gly Thr Arg Gln Leu Gly Ile Pro
 65 70 75 80

Thr Val Val Asp Arg Leu Ile Gln Gln Ala Ile Leu Gln Glu Leu Thr
 85 90 95

Pro Ile Phe Asp Pro Asp Phe Ser Pro Ser Ser Phe Gly Phe Arg Pro
 100 105 110

Gly Arg Asn Ala His Asp Ala Val Arg Gln Ala Gln Gly Tyr Ile Gln
 115 120 125

Glu Gly Tyr Arg Tyr Val Val Asp Met Asp Leu Glu Lys Phe Phe Asp

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130		135		140											
Arg 145	Val	Asn	His	Asp	Ile 150	Leu	Met	Ser	Arg	Val 155	Ala	Arg	Lys	Val	Lys 160
Asp	Lys	Arg	Val	Leu 165	Lys	Leu	Ile	Arg	Ala 170	Tyr	Leu	Gln	Ala	Gly 175	Val
Met	Ile	Glu	Gly 180	Val	Lys	Val	Gln	Thr 185	Glu	Glu	Gly	Thr	Pro 190	Gln	Gly
Gly	Pro	Leu 195	Ser	Pro	Leu	Leu	Ala 200	Asn	Ile	Leu	Leu	Asp 205	Asp	Leu	Asp
Lys	Glu 210	Leu	Glu	Lys	Arg	Gly 215	Leu	Lys	Phe	Cys	Arg 220	Tyr	Ala	Asp	Asp
Cys 225	Asn	Ile	Tyr	Val	Lys 230	Ser	Leu	Arg	Ala	Gly 235	Gln	Arg	Val	Lys	Gln 240
Ser	Ile	Gln	Arg	Phe 245	Leu	Glu	Lys	Thr	Leu 250	Lys	Leu	Lys	Val	Asn 255	Glu
Glu	Lys	Ser	Ala 260	Val	Asp	Arg	Pro	Trp 265	Lys	Arg	Ala	Phe	Leu 270	Gly	Phe
Ser	Phe	Thr 275	Pro	Glu	Arg	Lys	Ala 280	Arg	Ile	Arg	Leu	Ala 285	Pro	Arg	Ser
Ile	Gln 290	Arg	Leu	Lys	Gln	Arg 295	Ile	Arg	Gln	Leu	Thr 300	Asn	Pro	Asn	Trp
Ser 305	Ile	Ser	Met	Pro	Glu 310	Arg	Ile	His	Arg	Val 315	Asn	Gln	Tyr	Val	Met 320
Gly	Trp	Ile	Gly	Tyr 325	Phe	Arg	Leu	Val	Glu 330	Thr	Pro	Ser	Val	Leu 335	Gln
Thr	Ile	Glu	Gly 340	Trp	Ile	Arg	Arg	Arg 345	Leu	Arg	Leu	Cys	Gln 350	Trp	Leu
Gln	Trp	Lys 355	Arg	Val	Arg	Thr	Arg 360	Ile	Arg	Glu	Leu	Arg 365	Ala	Leu	Gly

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 Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg Lys Gly Ala
 370 375 380

Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu Gly Lys Thr
 385 390 395 400

Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg Tyr Phe Glu
 405 410 415

Leu Arg Gln Gly
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<210> 3
 <211> 1370
 <212> DNA
 <213> Artificial

<220>
 <223> Plasmid construct

<220>
 <221> misc_feature
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 aacgcattctt agcgagagac aacctcatca cggcgctcaa acgggtcgaa gccaaccaag 180
 gagcaccggg aatcgacgga gtatcaaccg atcaactccg tgattacatc cgcgctcact 240
 ggagcacgat ccgcgccccaa ctcttgggcg gaacctaccg gccggcgccct gtccgcaggg 300
 tcggaatccc gaaaccgggc ggcggcacac ggcagctagg cattcccacc gtggtggacc 360
 ggctgatcca acaagccatt cttcaagaac tcacacccat ttctgatcca gacttctccc 420
 cttccagctt cggattccgt ccggggccgta acgcccacga tgccgtgcgg caagcgcaag 480
 gctacatcca ggaagggtat cggtacgtgg tcgacatgga cctggaaaag ttctttgatc 540
 gggtaacca tgacatcttg atgagtcggg tggcccgaag agtcaaggat aaacgcgtgc 600
 tgaaactgat ccgtgcctac ctgcaagccg gcgttatgat cgaaggggtg aaggtgcaga 660
 cggaggaagg gacgccgcaa ggcggccccc tcagccccct gctggcgaac atccttctcg 720
 acgatttaga caaggaattg gagaagcgag gattgaaatt ctgccgttac gcagatgact 780
 gcaacatcta tgtgaaaagt ctgcgggcag gacaacgggt gaaacaaagc atccaacggt 840

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tcttggagaa aacgctcaaa ctcaaagtaa acgaggagaa aagtgcggtg gaccgcccgt	900
ggaaacgggc ctttctgggg tttagcttca caccggaacg aaaagcgcga atccggctcg	960
ccccaaaggtc gattcaacgt ctgaaacagc ggattcgaca gctgaccaac ccaaactgga	1020
gcatatcgat gccagaacga attcatcgcg tcaatcaata cgtcatggga tggatcgggt	1080
atcttcggct cgtcgaaacc ccgtctgtcc ttcagaccat cgaaggatgg attcggagga	1140
ggcttcgact ctgtcaatgg cttcaatgga aacgggtcag aaccagaatc cgtgagttaa	1200
gagcgctggg gctgaaagag acagcggtga tggagatcgc caatacccga aaaggagctt	1260
ggcgaacaac gaaaacgccg caactccacc aggccctggg caaacctac tggaccgctc	1320
aagggctcaa gagtttgacg caacgatatt tcgaactccg tcaaggttga	1370

<210> 4
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 <212> DNA
 <213> Artificial

<220>
 <223> Nucleotide primer containing NdeI restriction site

<220>
 <221> primer_bind
 <222> (1)..(32)

<400> 4	
agacaacata tgcggcaaga cctgaatctc at	32

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial

<220>
 <223> Nucleotide primer containing BamHI restriction site

<400> 5	
aatggatccg ctggcgaaca tccttctc	28

<210> 6
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 <212> DNA
 <213> Artificial

<220>
 <223> Nucleotide primer containing PstI restriction site

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<222> (1)..(29)

<400> 6
attactgcag agcgggtccag taggttttg

29

<210> 7
<211> 31
<212> DNA
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<223> Nucleotide primer containing HindIII restriction site

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<222> (1)..(31)

<400> 7
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<210> 8
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<212> PRT
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<223> Amino acid sequence of fusion protein

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<221> plasmid
<222> (1)..(455)

<220>
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<222> (1)..(455)

<400> 8

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Arg Gly Ser His Met Arg Gln Asp Leu Asn Leu Ile Pro Arg Lys Glu
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Lys Ile Thr Met Ala Leu Leu Glu Arg Ile Leu Ala Arg Asp Asn Leu
35 40 45

Ile Thr Ala Leu Lys Arg Val Glu Ala Asn Gln Gly Ala Pro Gly Ile
50 55 60

Asp Gly Val Ser Thr Asp Gln Leu Arg Asp Tyr Ile Arg Ala His Trp

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Leu Gly Phe Ser Phe Thr Pro Glu Arg Lys Ala Arg Ile Arg Leu Ala
 305 310 315 320

Pro Arg Ser Ile Gln Arg Leu Lys Gln Arg Ile Arg Gln Leu Thr Asn
 325 330 335

Pro Asn Trp Ser Ile Ser Met Pro Glu Arg Ile His Arg Val Asn Gln
 340 345 350

Tyr Val Met Gly Trp Ile Gly Tyr Phe Arg Leu Val Glu Thr Pro Ser
 355 360 365

Val Leu Gln Thr Ile Glu Gly Trp Ile Arg Arg Arg Leu Arg Leu Cys
 370 375 380

Gln Trp Leu Gln Trp Lys Arg Val Arg Thr Arg Ile Arg Glu Leu Arg
 385 390 395 400

Ala Leu Gly Leu Lys Glu Thr Ala Val Met Glu Ile Ala Asn Thr Arg
 405 410 415

Lys Gly Ala Trp Arg Thr Thr Lys Thr Pro Gln Leu His Gln Ala Leu
 420 425 430

Gly Lys Thr Tyr Trp Thr Ala Gln Gly Leu Lys Ser Leu Thr Gln Arg
 435 440 445

Tyr Phe Glu Leu Arg Gln Gly
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<210> 9
 <211> 25
 <212> DNA
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<220>
 <223> Primer sequence

<220>
 <221> prim_transcript
 <222> (1)..(25)

<400> 9
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25

<210> 10
 <211> 25

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<212> DNA
<213> Artificial

<220>
<223> Primer sequence

<220>
<221> prim_transcript
<222> (1)..(25)

<400> 10
tcaacactgt acggcacccg cattc

25

<210> 11
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Primer sequence

<220>
<221> prim_transcript
<222> (1)..(24)

<400> 11
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24